

32. (Reiterated) The method according to Claim 30, wherein said eukaryotic cell is a plant cell.

33. (Reiterated) The method according to Claim 32, wherein said plant cell is obtained from a plant selected from the group consisting of *Arabidopsis*, soybean, and corn.

REMARKS

Notice to Comply

The claims, specification and drawings must be amended to identify sequences by their SEQ ID NO.

Amendments

Amendments to the specification are being submitted as "clean" pages, with "marked-up" pages attached. Amendments to the claims are submitted above, with "marked-up" copies of the claims attached.

Applicants have amended page 4, paragraphs 1, 21 and 22, which refer to Figures 1, 21 and 22, respectively, by adding SEQ ID NOs which correspond with the listed sequences. Support for the amendment to paragraph 1 may be found on page 24, lines 3-4, and in Figure 1. Support for the amendment to paragraph 21 and 22 may be found in Figures 21 and 21, which list the specific amino acid sequences. Support for the changes to paragraphs 1, 21 and 22 may also be found in the computer readable sequence listing, as filed, which includes these sequences.

Applicants have amended page 34, paragraphs 2 and 3, which refer to Figures 22 and 23, by adding SEQ ID NOs which correspond with the listed sequences. Support for these amendments may be found in Figures 21 and 22, which list the specific amino acid sequences, and in the computer readable sequence listing, as filed, which includes these sequences.

Applicants have amended Claim 6 by deleting the phrase "the sequences of Figure 1" and adding specific reference to -- SEQ ID NOs: 2, 4, 6, 12 and 17-- . Support for this

amendment is found on page 24, lines 3-4 of the specification as filed, in Figure 1 as filed, which lists the sequences, and in the computer readable sequence listing, as filed, which includes the corresponding sequences.


Applicants have also amended Claim 19 to remove a superfluous semicolon.

CONCLUSION

If in the opinion of the Examiner, a telephone conference would expedite the prosecution of the subject application, the Examiner is invited to call the undersigned attorney at (650) 328-4400.

Respectfully submitted,

Dated: May 29, 2001


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Attachments

Changes to the Specification

On page 4, replace paragraph 1 (lines 3-4),

“Figure 1 provides an amino acid sequence alignment between ATPT2, ATPT3, ATPT4, ATPT8, and ATPT12 are performed using ClustalW.”

with the following:

--Figure 1 provides an amino acid sequence alignment between ATPT2, ATPT3, ATPT4, ATPT8, and ATPT12 (SEQ ID NOs: 2, 4, 6, 12 and 17, respectively), performed using ClustalW.--

On page 4, replace paragraph 21 (lines 24-25)

“Figure 21 provides an amino acid sequence alignment using ClustalW between the *Synechocystis* sequence knockouts .”

with the following:

--Figure 21 provides an amino acid sequence alignment using ClustalW between the *Synechocystis* sequence knockouts slr1736, slr0926, slr1899, slr0056, and slr1518 (SEQ ID NOs: 37, 32, 33, 34 and 35, respectively).--

On page 4, replace paragraph 22 (lines 26-28)

“Figure 22 provides an amino acid sequence of the ATPT2, ATPT3, ATPT4, ATPT8 and ATPT12 protein sequences from *Arabidopsis* (SEQ ID NOs: 2, 4, 6, 17 and 12, respectively) and the slr1736, slr0926, slr1899, slr0056, and the slr1518 amino acid sequences from *Synechocystis*.”

with the following:

--Figure 22 provides an amino acid sequence of the ATPT2, ATPT3, ATPT4, ATPT12 and ATPT8 protein sequences from *Arabidopsis* (SEQ ID NOs: 2, 4, 6, 17 and 12, respectively) and the slr1736, slr0926, slr1899, slr0056, and the slr1518 amino acid sequences from

Synechocystis (SEQ ID NOs: 37, 32, 33, 34 and 35, respectively).--

On page 34, replace paragraph 2 (lines 7-9)

“The amino acid sequences for the *Synechocystis* knockouts are compared using ClustalW, and are provided in Table 3 below. Provided are the percent identities, percent similarity, and the percent gap. The alignment of the sequences is provided in Figure 21.”
with the following:

--The amino acid sequences for the *Synechocystis* knockouts slr1736, slr0926, slr1899, slr0056 and slr1518 (SEQ ID NOs: 37, 32, 33, 34 and 35, respectively) are compared using ClustalW, and are provided in Table 3 below. Provided are the percent identities, percent similarity, and the percent gap. The alignment of the sequences is provided in Figure 21.--

Marked-up claims

The following “marked-up” claims are submitted in accordance with 37 C.F.R. 1.121.

6. (Amended) The DNA encoding sequence of Claim 5 wherein said prenyltransferase protein is encoded by a sequence selected from the group consisting of [the sequences of Figure 1] SEQ ID NOs: 2, 4, 6, 12 and 17.
19. (Amended) A method for the alteration of the tocopherol content in a host cell, comprising[;] transforming said host cell with a construct comprising as operably linked components, a transcriptional initiation region functional in a host cell, a nucleic acid sequence encoding prenyltransferase, and a transcriptional termination region.